

Sequence Listing

<110> Sang-Seok KOH
Qing LIU
Hyun-Ho CHUNG
Wen ZENG
Bog-Man LEE
Si-Young SONG

<120> GENE FAMILIES ASSOCIATED WITH LIVER CANCER

<130> 1599-0275PUS1

<140> US 10/524,530
<141> 2005-02-11

<150> US 60/402,905
<151> 2002-08-14

<150> US 60/403,651
<151> 2002-08-16

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<170> KopatentIn 1.71

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<212> DNA
<213> Homo sapiens

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accggattgt tttcgctggc ccagtgtccc cggagcttgt gtgcgataaca gagagcacct 120
cggaagctga ggcagctggt acttgacaga gagg atg gcg ctg tcg acc 169
Met Ala Leu Ser Thr
1 5

ata gtc tcc cag agg aag cag ata aag cgg aag gct ccc cgt ggc ttt 217
Ile Val Ser Gin Arg Lys Gln Ile Lys Arg Lys Ala Pro Arg Gly Phe
10 15 20

cta aag cga gtc ttc aag cga aag aag cct caa ctt cgt ctg gag aaa 265
Leu Lys Arg Val Phe Lys Arg Lys Lys Pro Gin Leu Arg Leu Glu Lys
25 30 35

agt ggt gac tta ttg gtc cat ctg aac tgt tta ctg ttt gtt cat cga 313
Ser Gly Asp Leu Leu Val His Leu Asn Cys Leu Leu Phe Val His Arg
40 45 50

tta gca gaa gag tcc agg aca aac gct tgt gcg agt aaa tgt aga gtc 361
Leu Ala Glu Glu Ser Arg Thr Asn Ala Cys Ala Ser Lys Cys Arg Val
55 60 65

att aac aag gag cat gta ctg gcc gca gca aag gta att cta aag aag 409
Ile Asn Lys Glu His Val Leu Ala Ala Lys Val Ile Leu Lys Lys
70 75 80 85

agc aga ggt ta gaagtcaaag aacatattct tgaaagttat gatgcattct 460
Ser Arg Gly

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atattggcta taaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 578

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Leu Arg Leu Glu Lys Ser Gly Asp Leu Leu Val His Leu Asn Cys Leu 35 40 45

Leu Phe Val His Arg Leu Ala Glu Glu Ser Arg Thr Asn Ala Cys Ala 50 55 60

Ser Lys Cys Arg Val Ile Asn Lys Glu His Val Leu Ala Ala Ala Lys 65 70 75 80

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120

tggtaacttga cagagagg .atg gcg ctg tcg acc ata gtc tcc cag agg aag			171
Met Ala Leu Ser Thr Ile Val Ser Gln Arg Lys			
1	5	10	
cag ata aag cgg aag gct ccc cgt ggc ttt cta aag cga gtc ttc aag			219
Gln Ile Lys Arg Lys Ala Pro Arg Gly Phe Leu Lys Arg Val Phe Lys			
15	20	25	
cta aag aag cct caa ctt cgt ctg gag aaa agt ggt gac tta ttg gtc			267
Leu Lys Pro Gln Leu Arg Leu Glu Lys Ser Gly Asp Leu Leu Val			
30	35	40	
cat ctg aac tgt tta ctg ttt gtt cat cga tta gca gaa gag tcc agg			315
His Leu Asn Cys Leu Leu Phe Val His Arg Leu Ala Glu Glu Ser Arg			
45	50	55	
aca aac gct tgt gcg agt aaa tgt aga gtc att aac aag gag cat gta			363
Thr Asn Ala Cys Ala Ser Lys Cys Arg Val Ile Asn Lys Glu His Val			
60	65	70	75
ctg gcc gca gca aag gta att cta aag aag agc aga ggt		tagaagtc	410
Leu Ala Ala Ala Lys Val Ile Leu Lys Ser Arg Gly			
80	85		
aaagaacata ttcttgaaag ttatgatgca ttctttggg tggtaacaga tcataaagac			470
atttttaca catcagttaa tatgggattta ttaaatattt gatataaaaaaaa aaaaaaaaaaa			530
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Leu Arg Leu Glu Lys Ser Gly Asp Leu Leu Val His Leu Asn Cys Leu			
35	40	45	
Leu Phe Val His Arg Leu Ala Glu Glu Ser Arg Thr Asn Ala Cys Ala			
50	55	60	
Ser Lys Cys Arg Val Ile Asn Lys Glu His Val Leu Ala Ala Ala Lys			
65	70	75	80
Val Ile Leu Lys Lys Ser Arg Gly			
85			

Leu Met Val Cys Ile Val Ile Gly Ala Arg Lys Leu Gly Val Asn Pro			
170	175	180	
gac aac att gcc acg ccc att gca gcc agc ctg gga gac ctc atc aca			622
Asp Asn Ile Ala Thr Pro Ile Ala Ala Ser Leu Gly Asp Leu Ile Thr			
185	190	195	
ctg tcc att ctg gct ttg gtt agc agc ttc ttc tac aga cac aaa gat			670
Leu Ser Ile Leu Ala Leu Val Ser Ser Phe Phe Tyr Arg His Lys Asp			
200	205	210	
agt cggttat ctg acg ccg ctg gtc tgc ctc agc ttt gcg gct ctg acc			718
Ser Arg Tyr Leu Thr Pro Leu Val Cys Leu Ser Phe Ala Ala Leu Thr			
215	220	225	
cca gtg tgg gtc ctc att gcc aag cag agc cca ccc atc gtg aag atc			766
Pro Val Trp Val Leu Ile Ala Lys Gln Ser Pro Pro Ile Val Lys Ile			
230	235	240	245
ctg aag ttt ggc tgg ttc cca atc atc ctg gcc atg gtc atc agc agt			814
Leu Lys Phe Gly Trp Phe Pro Ile Ile Leu Ala Met Val Ile Ser Ser			
250	255	260	
tgc gga gga ctc atc ttg agc aaa acc gtt tct aaa cag cag tac aaa			862
Phe Gly Gly Leu Ile Leu Ser Lys Thr Val Ser Lys Gln Gln Tyr Lys			
265	270	275	
ggc atg gcg ata ttt acc ccc gtc ata tgt ggt gtt ggc aat ctg			910
Gly Met Ala Ile Phe Thr Pro Val Ile Cys Gly Val Gly Gly Asn Leu			
280	285	290	
gtg gcc att cag acc agc cga atc tca acc tac ctg cac atg tgg agt			958
Val Ala Ile Gln Thr Ser Arg Ile Ser Thr Tyr Leu His Met Trp Ser			
295	300	305	
gca cct ggc gtc ctg ccc ctc cag atg aag aaa ttc tgg ccc aac ccg			1006
Ala Pro Gly Val Leu Pro Leu Gln Met Lys Lys Phe Trp Pro Asn Pro			
310	315	320	325
tgt tct act ttc tgc acg tca gaa atc aat tcc atg tca gct cga gtc			1054
Cys Ser Thr Phe Cys Thr Ser Glu Ile Asn Ser Met Ser Ala Arg Val			
330	335	340	
ctg ctc ttg ctg gtg gtc cca ggc cat ctg att ttc ttc tac atc atc			1102
Leu Leu Leu Val Val Pro Gly His Leu Ile Phe Phe Tyr Ile Ile			
345	350	355	
tac ctg gtg gag ggt cag tca gtc ata aac agc cag acc ttt gtg gtg			1150
Tyr Leu Val Glu Gly Gln Ser Val Ile Asn Ser Gln Thr Phe Val Val			
360	365	370	
ctc tac ctg ctg gca ggc ctg atc cag gtg aca atc ctg ctg tac ctg			1198
Leu Tyr Leu Leu Ala Gly Leu Ile Gln Val Thr Ile Leu Leu Tyr Leu			
375	380	385	
gca gaa gtg atg gtt cgg ctg act tgg cac cag gcc ctg gat cct gac			1246
Ala Glu Val Met Val Arg Leu Thr Trp His Gln Ala Leu Asp Pro Asp			

390	395	400	405	
aac cac tgc atc ccc tac ctt aca ggg ctg ggg gac ctg ctc ggt act				1294
Asn His Cys Ile Pro Tyr Leu Thr Gly Leu Gly Asp Leu Leu Gly Thr				
410	415	420		
ggc ctc ctg gca ctc tgc ttt ttc act gac tgg cta ctg aag agc aag				1342
Gly Leu Leu Ala Leu Cys Phe Phe Thr Asp Trp Leu Leu Lys Ser Lys				
425	430	435		
gca gag ctg ggt ggc atc tca gaa ctg gca tct gga cct ccc	taactg			1390
Ala Glu Leu Gly Gly Ile Ser Glu Leu Ala Ser Gly Pro Pro				
440	445	450		
ggccccgctg gtcccatatttgc tcatttagaa ttccctctca catcagtggg atacagaatt				1450
cagtttctcc cttgccaggat ccttgggatg gttgaccctt gcctctgcag tagccttttg				1510
ttagtctgct aaggttagctc tcacacaccc tggctctggg gttgataacct gagcctgcaa				1570
tagagccctg aaatcaagag catggcttga gtgtgtgaat atgatgtgtg cacatgctta				1630
atgagcgtgc aagtgtgcac acgtttgtgg agaggagggt gttctggcct gagaaggtaa				1690
agaagaggca tgtccagtat gctttgcagg gtgtgttg tctttccat gcccattgcaa				1750
cccaaggattgg ggtggagcag gaaggagctc ttttctgttc ccaaggctca gaactcttga				1810
gttgtggctt acttgcgtgc ttccaccaggat tcaagctccg tggccacac tgctgctgtg				1870
ccaagaagggt gtacagccctc cccaggatgg ggcctcatac aacccttcat ctgactcaa				1930
catttaatcg tgtccttgct gtcttttat ttccctttt gtttgttagc aaaaacctct				1990
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aaaaaaaaaaaa aaaaaaaaaa				2067

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<213> Homo sapiens

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Pro Gly Glu Leu Gly Leu Pro His Pro Leu Ser Thr Gly Gly Leu Pro
20 25 30

Val Ala Ser Glu Asp Gly Ala Leu Arg Ala Pro Glu Ser Gln Ser Val
35 40 45

Thr Pro Lys Pro Leu Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser
50 55 60

Ile	Gly	Leu	Gln	Val	Thr	Val	Pro	Phe	Met	Phe	Ala	Gly	Leu	Gly	Leu
65															80
Ser	Trp	Ala	Gly	Met	Leu	Leu	Asp	Tyr	Phe	Gln	Ala	Asn	Thr	Gly	Gln
				85					90						95
Ile	Asp	Asp	Pro	Gln	Glu	Gln	His	Arg	Val	Ile	Ser	Ser	Asn	Leu	Ala
				100					105						110
Leu	Ile	Gln	Val	Gln	Ala	Thr	Val	Val	Gly	Leu	Leu	Ala	Ala	Val	Ala
				115				120							125
Ala	Leu	Leu	Leu	Gly	Val	Val	Ser	Arg	Glu	Glu	Val	Asp	Val	Ala	Lys
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Val	Glu	Leu	Leu	Cys	Ala	Ser	Ser	Val	Leu	Thr	Ala	Phe	Leu	Ala	Ala
				145				150				155			160
Phe	Ala	Leu	Gly	Val	Leu	Met	Val	Cys	Ile	Val	Ile	Gly	Ala	Arg	Lys
				165					170						175
Leu	Gly	Val	Asn	Pro	Asp	Asn	Ile	Ala	Thr	Pro	Ile	Ala	Ala	Ser	Leu
				180					185						190
Gly	Asp	Leu	Ile	Thr	Leu	Ser	Ile	Leu	Ala	Leu	Val	Ser	Ser	Phe	Phe
				195				200							205
Tyr	Arg	His	Lys	Asp	Ser	Arg	Tyr	Leu	Thr	Pro	Leu	Val	Cys	Leu	Ser
				210			215								220
Phe	Ala	Ala	Leu	Thr	Pro	Val	Trp	Val	Leu	Ile	Ala	Lys	Gln	Ser	Pro
				225				230				235			240
Pro	Ile	Val	Lys	Ile	Leu	Lys	Phe	Gly	Trp	Phe	Pro	Ile	Ile	Leu	Ala
				245					250						255
Met	Val	Ile	Ser	Ser	Phe	Gly	Gly	Leu	Ile	Leu	Ser	Lys	Thr	Val	Ser
				260					265						270
Lys	Gln	Gln	Tyr	Lys	Gly	Met	Ala	Ile	Phe	Thr	Pro	Val	Ile	Cys	Gly
				275				280							285
Val	Gly	Gly	Asn	Leu	Val	Ala	Ile	Gln	Thr	Ser	Arg	Ile	Ser	Thr	Tyr
				290				295							300
Leu	His	Met	Trp	Ser	Ala	Pro	Gly	Val	Leu	Pro	Leu	Gln	Met	Lys	Lys
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Phe	Trp	Pro	Asn	Pro	Cys	Ser	Thr	Phe	Cys	Thr	Ser	Glu	Ile	Asn	Ser
				325					330						335
Met	Ser	Ala	Arg	Val	Leu	Leu	Leu	Val	Val	Pro	Gly	His	Leu	Ile	
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Phe	Phe	Tyr	Ile	Ile	Tyr	Leu	Val	Glu	Gly	Gln	Ser	Val	Ile	Asn	Ser
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Gln Thr Phe Val Val Leu Tyr Leu Leu Ala Gly Leu Ile Gln Val Thr
370 375 380

Ile Leu Leu Tyr Leu Ala Glu Val Met Val Arg Leu Thr Trp His Gln
385 390 395 400

Ala Leu Asp Pro Asp Asn His Cys Ile Pro Tyr Leu Thr Gly Leu Gly
405 410 415

Asp Leu Leu Gly Thr Gly Leu Leu Ala Leu Cys Phe Phe Thr Asp Trp
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Leu Leu Lys Ser Lys Ala Glu Leu Gly Gly Ile Ser Glu Leu Ala Ser
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Gly Pro Pro
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<210> 7
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<223> Clone MB5

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Thr Arg Gln Arg Arg Leu Asp Ser Cys Gly Lys Pro Gly Glu Leu Gly
10 15 20

ctt cct cac ccc ctc agc aca gga gga ctc cct gta gcc tca gaa gat 151
Leu Pro His Pro Leu Ser Thr Gly Gly Leu Pro Val Ala Ser Glu Asp
25 30 35

gga gct ctc agg gcc cct gag agc caa agc gtg acc ccc aag cca ctg 199
Gly Ala Leu Arg Ala Pro Glu Ser Gln Ser Val Thr Pro Lys Pro Leu
40 45 50

gag act gag cct agc agg gag acc gcc tgg tcc ata ggc ctt cag gtg 247
Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser Ile Gly Leu Gln Val
55 60 65

acc gtg ccc ttc atg ttt gca ggc ctg gga ctg tcc tgg gcc ggc atg 295
Thr Val Pro Phe Met Phe Ala Gly Leu Gly Leu Ser Trp Ala Gly Met
70 75 80 85

ctt ctg gac tat ttc cag cac tgg cct gtg ttt gtg gag gtg aaa gac 343
Leu Leu Asp Tyr Phe Gln His Trp Pro Val Phe Val Glu Val Lys Asp

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atg aca ctg gca tcc aga ctc tcc aca gct gcc aac act gga caa att Met Thr Leu Ala Ser Arg Leu Ser Thr Ala Ala Asn Thr Gly Gln Ile 120	125	130	439
gat gac ccc cag gag cag cac aga gtc atc agc agc aac ctg gcc ctc Asp Asp Pro Gln Glu Gln His Arg Val Ile Ser Ser Asn Leu Ala Leu 135	140	145	487
atc cag gtg cag gcc act gtc gtg ggg ctc ttg gct gct gtg gct gcg Ile Gln Val Gln Ala Thr Val Val Gly Leu Leu Ala Ala Val Ala Ala 150	155	160	535
ctg ctg ttg ggc gtg gtg tct cga gag gaa gtg gat gtc gcc aag gtg Leu Leu Leu Gly Val Val Ser Arg Glu Glu Val Asp Val Ala Lys Val 170	175	180	583
gag ttg ctg tgt gcc agc agt gtc ctc act gcc ttc ctt gca gcc ttt Glu Leu Leu Cys Ala Ser Ser Val Leu Thr Ala Phe Leu Ala Ala Phe 185	190	195	631
gcc ctg ggg gtg ctg atg gtc tgt ata gtg att ggt gct cga aag ctc Ala Leu Gly Val Leu Met Val Cys Ile Val Ile Gly Ala Arg Lys Leu 200	205	210	679
ggg gtc aac cca gac aac att gcc acg ccc att gca gcc agc ctg gga Gly Val Asn Pro Asp Asn Ile Ala Thr Pro Ile Ala Ala Ser Leu Gly 215	220	225	727
gac ctc atc aca ctg tcc att ctg gct ttg gtt agc agc ttc ttc tac Asp Leu Ile Thr Leu Ser Ile Leu Ala Leu Val Ser Ser Phe Phe Tyr 230	235	240	775
aga cac aaa gat agt cgg tat ctg acg ccg ctg gtc tgc ctc agc ttt Arg His Lys Asp Ser Arg Tyr Leu Thr Pro Leu Val Cys Leu Ser Phe 250	255	260	823
gcg gct ctg acc cca gtg tgg gtc ctc att gcc aag cag agc cca ccc Ala Ala Leu Thr Pro Val Trp Val Leu Ile Ala Lys Gln Ser Pro Pro 265	270	275	871
atc gtg aag atc ctg aag ttt ggc tgg ttc cca atc atc ctg gcc atg Ile Val Lys Ile Leu Lys Phe Gly Trp Phe Pro Ile Ile Leu Ala Met 280	285	290	919
gtc atc agc agt ttc gga gga ctc atc ttg agc aaa acc gtt tct aaa Val Ile Ser Ser Phe Gly Gly Leu Ile Leu Ser Lys Thr Val Ser Lys 295	300	305	967
cag cag tac aaa ggc atg gcg ata ttt acc ccc gtc ata tgt ggt gtt Gln Gln Tyr Lys Gly Met Ala Ile Phe Thr Pro Val Ile Cys Gly Val 310	315	320	1015

ggt ggc aat ctg gtg gcc att cag acc agc cga atc tca acc tac ctg Gly Gly Asn Leu Val Ala Ile Gln Thr Ser Arg Ile Ser Thr Tyr Leu 330 335 340	1063
cac atg tgg agt gca cct ggc gtc ctg ccc ctc cag atg aag aaa ttc His Met Trp Ser Ala Pro Gly Val Leu Pro Leu Gln Met Lys Lys Phe 345 350 355	1111
tgg ccc aac ccg tgt tct act ttc tgc acg tca gaa atc aat tcc atg Trp Pro Asn Pro Cys Ser Thr Phe Cys Thr Ser Glu Ile Asn Ser Met 360 365 370	1159
tca gct cga gtc ctc ttg ctg gtg gtc cca ggc cat ctg att ttc Ser Ala Arg Val Leu Leu Leu Val Val Pro Gly His Leu Ile Phe 375 380 385	1207
ttc tac atc atc tac ctg gtg gag ggt cag tca gtc ata aac agc cag Phe Tyr Ile Ile Tyr Leu Val Glu Gly Gln Ser Val Ile Asn Ser Gln 390 395 400 405	1255
acc ttt gtg gtg ctc tac ctg ctg gca ggc ctg atc cag gtg aca atc Thr Phe Val Val Leu Tyr Leu Leu Ala Gly Leu Ile Gln Val Thr Ile 410 415 420	1303
ctg ctg tac ctg gca gaa gtg atg gtt cgg ctg act tgg cac cag gcc Leu Leu Tyr Leu Ala Glu Val Met Val Arg Leu Thr Trp His Gln Ala 425 430 435	1351
ctg gat cct gac aac cac tgc atc ccc tac ctt aca ggg ctg ggg gac Leu Asp Pro Asp Asn His Cys Ile Pro Tyr Leu Thr Gly Leu Gly Asp 440 445 450	1399
ctg ctc ggt act ggc ctc ctg gca ctc tgc ttt ttc act gac tgg cta Leu Leu Gly Thr Gly Leu Leu Ala Leu Cys Phe Phe Thr Asp Trp Leu 455 460 465	1447
ctg aag agc aag gca gag ctg ggt ggc atc tca gaa ctg gca tct gga Leu Lys Ser Lys Ala Glu Leu Gly Gly Ile Ser Glu Leu Ala Ser Gly 470 475 480 485	1495
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tttccatgcc catgcaaccc agattgggtt ggagcaggaa ggagctctt tctgttcccc	1910
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 2090
 2150
 2178

<210> 8
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Pro Gly Glu Leu Gly Leu Pro His Pro Leu Ser Thr Gly Gly Leu Pro
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Val Ala Ser Glu Asp Gly Ala Leu Arg Ala Pro Glu Ser Gln Ser Val
 35 40 45

Thr Pro Lys Pro Leu Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser
 50 55 60

Ile Gly Leu Gln Val Thr Val Pro Phe Met Phe Ala Gly Leu Gly Leu
 65 70 75 80

Ser Trp Ala Gly Met Leu Leu Asp Tyr Phe Gln His Trp Pro Val Phe
 85 90 95

Val Glu Val Lys Asp Leu Leu Thr Leu Val Pro Pro Leu Val Gly Leu
 100 105 110

Lys Gly Asn Leu Glu Met Thr Leu Ala Ser Arg Leu Ser Thr Ala Ala
 115 120 125

Asn Thr Gly Gln Ile Asp Asp Pro Gln Glu Gln His Arg Val Ile Ser
 130 135 140

Ser Asn Leu Ala Leu Ile Gln Val Gln Ala Thr Val Val Gly Leu Leu
 145 150 155 160

Ala Ala Val Ala Ala Leu Leu Leu Gly Val Val Ser Arg Glu Glu Val
 165 170 175

Asp Val Ala Lys Val Glu Leu Leu Cys Ala Ser Ser Val Leu Thr Ala
 180 185 190

Phe Leu Ala Ala Phe Ala Leu Gly Val Leu Met Val Cys Ile Val Ile
 195 200 205

Gly Ala Arg Lys Leu Gly Val Asn Pro Asp Asn Ile Ala Thr Pro Ile
 210 215 220

Ala Ala Ser Leu Gly Asp Leu Ile Thr Leu Ser Ile Leu Ala Leu Val
 225 230 235 240

 Ser Ser Phe Phe Tyr Arg His Lys Asp Ser Arg Tyr Leu Thr Pro Leu
 245 250 255

 Val Cys Leu Ser Phe Ala Ala Leu Thr Pro Val Trp Val Leu Ile Ala
 260 265 270

 Lys Gln Ser Pro Pro Ile Val Lys Ile Leu Lys Phe Gly Trp Phe Pro
 275 280 285

 Ile Ile Leu Ala Met Val Ile Ser Ser Phe Gly Gly Leu Ile Leu Ser
 290 295 300

 Lys Thr Val Ser Lys Gln Gln Tyr Lys Gly Met Ala Ile Phe Thr Pro
 305 310 315 320

 Val Ile Cys Gly Val Gly Gly Asn Leu Val Ala Ile Gln Thr Ser Arg
 325 330 335

 Ile Ser Thr Tyr Leu His Met Trp Ser Ala Pro Gly Val Leu Pro Leu
 340 345 350

 Gin Met Lys Lys Phe Trp Pro Asn Pro Cys Ser Thr Phe Cys Thr Ser
 355 360 365

 Glu Ile Asn Ser Met Ser Ala Arg Val Leu Leu Leu Val Val Pro
 370 375 380

 Gly His Leu Ile Phe Phe Tyr Ile Ile Tyr Leu Val Glu Gly Gln Ser
 385 390 395 400

 Val Ile Asn Ser Gln Thr Phe Val Val Leu Tyr Leu Leu Ala Gly Leu
 405 410 415

 Ile Gin Val Thr Ile Leu Leu Tyr Leu Ala Glu Val Met Val Arg Leu
 420 425 430

 Thr Trp His Gln Ala Leu Asp Pro Asp Asn His Cys Ile Pro Tyr Leu
 435 440 445

 Thr Gly Leu Gly Asp Leu Leu Gly Thr Gly Leu Leu Ala Leu Cys Phe
 450 455 460

 Phe Thr Asp Trp Leu Leu Lys Ser Lys Ala Glu Leu Gly Gly Ile Ser
 465 470 475 480

 Glu Leu Ala Ser Gly Pro Pro
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 <222> (31)..(1551)
 <223> Clone IE4

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cg	agg	ctg	gac	agc	tgt	ggc	aag	cca	ggg	gag	ctg	ggg	ctt	cct	cac	102
Arg	Arg	Leu	Asp	Ser	Cys	Gly	Lys	Pro	Gly	Glu	Leu	Gly	Leu	Pro	His	
10		15									20					
ccc	ctc	agc	aca	gga	gga	ctc	cct	gta	gcc	tca	gaa	gat	gga	gct	ctc	150
Pro	Leu	Ser	Thr	Gly	Gly	Leu	Pro	Val	Ala	Ser	Glu	Asp	Gly	Ala	Leu	
25		30									35		40			
agg	gcc	cct	gag	agc	caa	agc	gtg	acc	ccc	aag	cca	ctg	gag	act	gag	198
Arg	Ala	Pro	Glu	Ser	Gln	Ser	Val	Thr	Pro	Lys	Pro	Leu	Glu	Thr	Glu	
45		50									55					
cct	agc	agg	gag	acc	gcc	tgg	tcc	ata	ggc	ctt	cag	gtg	acc	gtg	ccc	246
Pro	Ser	Arg	Glu	Thr	Ala	Trp	Ser	Ile	Gly	Leu	Gln	Val	Thr	Val	Pro	
60		65									70					
ttc	atg	ttt	gca	ggc	ctg	gga	ctg	tcc	tgg	gcc	atg	ctt	ctg	gac	294	
Phe	Met	Phe	Ala	Gly	Leu	Gly	Leu	Ser	Trp	Ala	Gly	Met	Leu	Leu	Asp	
75		80									85					
tat	ttc	cag	cac	tgg	cct	gtg	ttt	gtg	gag	gtg	aaa	gac	ctt	ttg	aca	342
Tyr	Phe	Gln	His	Trp	Pro	Val	Phe	Val	Glu	Val	Lys	Asp	Leu	Leu	Thr	
90		95									100					
ttg	gtg	ccg	ccc	ctg	gtg	ggc	ctg	aag	ggg	aac	ctg	gag	atg	aca	ctg	390
Leu	Val	Pro	Pro	Leu	Val	Gly	Leu	Lys	Gly	Asn	Leu	Glu	Met	Thr	Leu	
105		110									115		120			
gca	tcc	aga	ctc	tcc	aca	gct	gcc	aac	act	gga	caa	att	gat	gac	ccc	438
Ala	Ser	Arg	Leu	Ser	Thr	Ala	Ala	Asn	Thr	Gly	Gln	Ile	Asp	Asp	Pro	
125		130									130		135			
cag	gag	cag	cac	aga	gtc	atc	agc	agc	aac	ctg	gcc	ctc	atc	cag	gtg	486
Gln	Gln	His	Arg	Val	Ile	Ser	Ser	Asn	Leu	Ala	Leu	Ile	Gln	Val		
140		145									150					
cag	gcc	act	gtc	gtg	ggg	ctc	ttg	gct	gtg	gct	gcg	ctg	ctg	ttg	534	
Gln	Ala	Thr	Val	Val	Gly	Leu	Leu	Ala	Ala	Val	Ala	Ala	Leu	Leu	Leu	
155		160									165					
ggc	gtg	gtg	tct	cga	gag	gaa	gtg	gat	gtc	gcc	aag	gtg	gag	ttg	ctg	582
Gly	Val	Val	Ser	Arg	Glu	Glu	Val	Asp	Val	Ala	Lys	Val	Glu	Leu	Leu	
170		175									180					
tgt	gcc	agc	agt	gtc	ctc	act	gcc	ttc	ctt	gca	gcc	ttt	gcc	ctg	ggg	630

Cys Ala Ser Ser Val Leu Thr Ala Phe Leu Ala Ala Phe Ala Leu Gly			
185	190	195	200
gtg ctg atg gtc tgt ata gtg att ggt gct cga aag ctc ggg gtc aac			678
Val Leu Met Val Cys Ile Val Ile Gly Ala Arg Lys Leu Gly Val Asn			
205	210	215	
cca gac aac att gcc acg ccc att gca gcc agc ctg gga gac ctc atc			726
Pro Asp Asn Ile Ala Thr Pro Ile Ala Ala Ser Leu Gly Asp Leu Ile			
220	225	230	
aca ctg tcc att ctg gct ttg gtt agc agc ttc ttc tac aga cac aaa			774
Thr Leu Ser Ile Leu Ala Leu Val Ser Ser Phe Phe Tyr Arg His Lys			
235	240	245	
gat agt cgg tat ctg acg ccg ctg gtc tgc ctc agc ttt gcg gct ctg			822
Asp Ser Arg Tyr Leu Thr Pro Leu Val Cys Leu Ser Phe Ala Ala Leu			
250	255	260	
acc cca gtg tgg gtc ctc att gcc aag cag agc cca ccc atc gtg aag			870
Thr Pro Val Trp Val Leu Ile Ala Lys Gln Ser Pro Pro Ile Val Lys			
265	270	275	280
atc ctg aag ttt ggc tgg ttc cca atc atc ctg gcc atg gtc atc agc			918
Ile Leu Lys Phe Gly Trp Phe Pro Ile Ile Leu Ala Met Val Ile Ser			
285	290	295	
agt ttc gga gga ctc atc ttg agc aaa acc gtt tct aaa cag cag tac			966
Ser Phe Gly Gly Leu Ile Leu Ser Lys Thr Val Ser Lys Gln Gln Tyr			
300	305	310	
aaa ggc atg gcg ata ttt acc ccc gtc ata tgt ggt gtt ggt ggc aat			1014
Lys Gly Met Ala Ile Phe Thr Pro Val Ile Cys Gly Val Gly Gly Asn			
315	320	325	
ctg gtg gcc att cag acc agc cga atc tca acc tac ctg cac atg tgg			1062
Leu Val Ala Ile Gln Thr Ser Arg Ile Ser Thr Tyr Leu His Met Trp			
330	335	340	
agt gca cct ggc gtc ctg ccc ctc cag atg aag aaa ttc tgg ccc aac			1110
Ser Ala Pro Gly Val Leu Pro Leu Gln Met Lys Lys Phe Trp Pro Asn			
345	350	355	360
ccg tgt tct act ttc tgc acg tca gaa atc aat tcc atg tca gct cga			1158
Pro Cys Ser Thr Phe Cys Thr Ser Glu Ile Asn Ser Met Ser Ala Arg			
365	370	375	
gtc ctg ctc ttg ctg gtg gtc cca ggc cat ctg att ttc ttc tac atc			1206
Val Leu Leu Leu Val Val Pro Gly His Leu Ile Phe Phe Tyr Ile			
380	385	390	
atc tac ctg gtg gag ggt cag tca gtc ata aac agc cag acc ttt gtg			1254
Ile Tyr Leu Val Glu Gly Gln Ser Val Ile Asn Ser Gln Thr Phe Val			
395	400	405	
gtg cts tac ctg ctg gca ggc ctg atc cag gtg aca atc ctg ctg tac			1302
Val Leu Tyr Leu Leu Ala Gly Leu Ile Gln Val Thr Ile Leu Leu Tyr			

410	415	420	
ctg gca gaa gtg atg gtt cgg ctg act tgg cac cag gcc ctg gat cct Leu Ala Glu Val Met Val Arg Leu Thr Trp His Gln Ala Leu Asp Pro			1350
425	430	435	440
gac aac cac tgc atc ccc tac ctt aca ggg ctg ggg gac ctg ctc ggt Asp Asn His Cys Ile Pro Tyr Leu Thr Gly Leu Gly Asp Leu Leu Gly			1398
445	450		455
tca agc tcc gtg ggc cac act gct gct gtg cca aga agg tgt aca gcc Ser Ser Ser Val Gly His Thr Ala Ala Val Pro Arg Arg Cys Thr Ala			1446
460	465		470
tcc cca gga tgg ggc ctc ata caa ccc ttc atc tgc act caa cat tta Ser Pro Gly Trp Gly Leu Ile Gln Pro Phe Ile Cys Thr Gln His Leu			1494
475	480		485
atc gtg tcc ttg ctg tct ttt tat ttt cct ttt tgt ttg tta gca aaa Ile Val Ser Leu Leu Ser Phe Tyr Phe Pro Phe Cys Leu Leu Ala Lys			1542
490	495		500
acc tct att tagatttca ataatcagag aagtgtaaaa taaaacagat tatattgtaa Thr Ser Ile			1600
505			
aaaaaaaaaaaa aaaaaaa			1616
<210> 10			
<211> 507			
<212> PRT			
<213> Homo sapiens			
<400> 10			
Met Asp Gly Thr Glu Thr Arg Gln Arg Arg Leu Asp Ser Cys Gly Lys			
1	5	10	15
Pro Gly Glu Leu Gly Leu Pro His Pro Leu Ser Thr Gly Leu Pro			
20	25		30
Val Ala Ser Glu Asp Gly Ala Leu Arg Ala Pro Glu Ser Gln Ser Val			
35	40		45
Thr Pro Lys Pro Leu Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser			
50	55	60	
Ile Gly Leu Gln Val Thr Val Pro Phe Met Phe Ala Gly Leu Gly Leu			
65	70	75	80
Ser Trp Ala Gly Met Leu Leu Asp Tyr Phe Gln His Trp Pro Val Phe			
85	90		95
Val Glu Val Lys Asp Leu Leu Thr Leu Val Pro Pro Leu Val Gly Leu			
100	105		110
Lys Gly Asn Leu Glu Met Thr Leu Ala Ser Arg Leu Ser Thr Ala Ala			

115	120	125
Asn Thr Gly Gln Ile Asp Asp Pro Gln Glu Gln His Arg Val Ile Ser		
130	135	140
Ser Asn Leu Ala Leu Ile Gln Val Gln Ala Thr Val Val Gly Leu Leu		
145	150	155
Ala Ala Val Ala Ala Leu Leu Leu Gly Val Val Ser Arg Glu Glu Val		
165	170	175
Asp Val Ala Lys Val Glu Leu Leu Cys Ala Ser Ser Val Leu Thr Ala		
180	185	190
Phe Leu Ala Ala Phe Ala Leu Gly Val Leu Met Val Cys Ile Val Ile		
195	200	205
Gly Ala Arg Lys Leu Gly Val Asn Pro Asp Asn Ile Ala Thr Pro Ile		
210	215	220
Ala Ala Ser Leu Gly Asp Leu Ile Thr Leu Ser Ile Leu Ala Leu Val		
225	230	235
Ser Ser Phe Phe Tyr Arg His Lys Asp Ser Arg Tyr Leu Thr Pro Leu		
245	250	255
Val Cys Leu Ser Phe Ala Ala Leu Thr Pro Val Trp Val Leu Ile Ala		
260	265	270
Lys Gln Ser Pro Pro Ile Val Lys Ile Leu Lys Phe Gly Trp Phe Pro		
275	280	285
Ile Ile Leu Ala Met Val Ile Ser Ser Phe Gly Gly Leu Ile Leu Ser		
290	295	300
Lys Thr Val Ser Lys Gln Gln Tyr Lys Gly Met Ala Ile Phe Thr Pro		
305	310	315
320		
Val Ile Cys Gly Val Gly Gly Asn Leu Val Ala Ile Gln Thr Ser Arg		
325	330	335
Ile Ser Thr Tyr Leu His Met Trp Ser Ala Pro Gly Val Leu Pro Leu		
340	345	350
Gln Met Lys Lys Phe Trp Pro Asn Pro Cys Ser Thr Phe Cys Thr Ser		
355	360	365
Glu Ile Asn Ser Met Ser Ala Arg Val Leu Leu Leu Val Val Pro		
370	375	380
Gly His Leu Ile Phe Phe Tyr Ile Ile Tyr Leu Val Glu Gly Gln Ser		
385	390	395
400		
Val Ile Asn Ser Gln Thr Phe Val Val Leu Tyr Leu Leu Ala Gly Leu		
405	410	415
Ile Gln Val Thr Ile Leu Leu Tyr Leu Ala Glu Val Met Val Arg Leu		

420

425

430

Thr Trp His Gln Ala Leu Asp Pro Asp Asn His Cys Ile Pro Tyr Leu
435 440 445

Thr Gly Leu Gly Asp Leu Leu Gly Ser Ser Ser Val Gly His Thr Ala
450 455 460

Ala Val Pro Arg Arg Cys Thr Ala Ser Pro Gly Trp Gly Leu Ile Gln
465 470 475 480

Pro Phe Ile Cys Thr Gln His Leu Ile Val Ser Leu Leu Ser Phe Tyr
485 490 495

Phe Pro Phe Cys Leu Leu Ala Lys Thr Ser Ile
500 505